

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

- (i) APPLICANT: Sato, Takaaki
- 10 (ii) TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
- (iii) NUMBER OF SEQUENCES: 37
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
20 (D) STATE: New York
(E) COUNTRY: U.S.A
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/51902-A-PCT
- 40 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525

45 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3479 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 55 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 458..3211
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CCTGATCGTT	GGTAGTGGCA	TGGAGGACGG	GGCTGGCATT	TCAGACTGCC	AGCTGTTTTT	60
	ACCAGCCGCT	GCATCACTTG	AATAGAAGCT	ATGCATATTG	GCTGGCCGAC	AAAGCCAAGG	120
	5GACAAAAGCT	ATGGCCGTTA	AAATGGTCCC	TCTGAGTCCA	GGGCTCTTTC	CCTGGCTTTT	180
	AGCACCATGG	ATCTCTTCCT	TTTCATCCCA	TCAGCAATGT	GGTACCTTCT	TCTACTTGAT	240
	GATGACAGCT	GATACTTCAG	ATTTGCCTGA	CTAAGGTTAG	AAACCTGAAT	CGCTGTGAGG	300
10	AAGATGAAAT	TTCCATTTTA	CTTGGTGCCT	TGTGCAGGGA	GCACACTGAT	CCTTCCAGAA	360
	ACTTGTGTGT	GAAAAGAGGT	TGCGTTTTGT	CAGACAGACT	CATGGTTATG	GCGAGCGATC	420
15	CGACGTGATC	AGAGTGGGCA	AGAGGCACAG	CGAACTC	ATG ACA	GGC TAT ACC ATG	475
					Met Thr Gly Tyr Thr Met		
					1	5	
	TTG CGG AAT GGG GGA GTG GGG AAC GGT GGT CAG ACC TGT ATG CTG CGC	523					
20	Leu Arg Asn Gly Gly Val Gly Asn Gly Gly Gln Thr Cys Met Leu Arg						
		10	15	20			
	TGG TCC AAT CGC ATC CGG CTG ACA TGG CTG AGT TTC ACG CTG TTC ATC	571					
25	Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser Phe Thr Leu Phe Ile						
		25	30	35			
	ATC CTC GTC TTC TTC CCC CTC ATT GCT CAC TAT TAC CTC ACC ACT CTG	619					
30	Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr Tyr Leu Thr Thr Leu						
		40	45	50			
	GAC GAG GCA GAC GAG GCT GGC AAG CGC ATC TTC GGC CCT CGG GCT GGC	667					
	Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe Gly Pro Arg Ala Gly						
		55	60	65	70		
35	AGT GAG CTC TGT GAG GTA AAG CAT GTC CTT GAT CTC TGT CGG ATT CGT	715					
	Ser Glu Leu Cys Glu Val Lys His Val Leu Asp Leu Cys Arg Ile Arg						
		75	80	85			
	GAG TCT GTG AGC GAA GAG CTT CTA CAG CTC GAA GCC AAG CGG CAG GAG	763					
40	Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu Ala Lys Arg Gln Glu						
		90	95	100			
	CTG AAC AGC GAG ATT GCC AAG CTG AAC CTC AAG ATT GAA GCC TGT AAG	811					
45	Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu Lys Ile Glu Ala Cys Lys						
		105	110	115			
	AAG AGC ATA GAG AAT GCC AAG CAG GAC CTG CTG CAG CTC AAG AAT GTC	859					
	Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu Leu Gln Leu Lys Asn Val						
		120	125	130			
50	ATT AGC CAG ACA GAG CAC TCC TAC AAG GAG CTG ATG GCC CAG AAC CAG	907					
	Ile Ser Gln Thr Glu His Ser Tyr Lys Glu Leu Met Ala Gln Asn Gln						
		135	140	145	150		
55	CCC AAA CTG TCC CTG CCC ATC CGA CTG CTC CCT GAG AAG GAC GAT GCC	955					
	Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu Pro Glu Lys Asp Asp Ala						
		155	160	165			
	GGC CTT CCA CCC CCC AAG GTC ACT CGG GGT TGC CGC CTT CAC AAC TGC	1003					
60	Gly Leu Pro Pro Pro Lys Val Thr Arg Gly Cys Arg Leu His Asn Cys						
		170	175	180			
	TTT GAT TAC TCT CGT TGT CCT CTG ACG TCT GGC TTT CCC GTC TAC GTC	1051					

Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser Gly Phe Pro Val Tyr Val
 185 190 195

TAT GAC AGT GAC CAG TTT GCC TTT GGG AGC TAC CTG GAC CCT TTG GTC 1099
 5Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser Tyr Leu Asp Pro Leu Val
 200 205 210

AAG CAG GCT TTT CAG GCT ACA GTG AGA GCC AAC GTT TAT GTT ACA GAA 1147
 Lys Gln Ala Phe Gln Ala Thr Val Arg Ala Asn Val Tyr Val Thr Glu
 10215 220 225 230

AAT GCG GCC ATC GCC TGC CTG TAT GTG GTG TTA GTG GGA GAA ATG CAA 1195
 Asn Ala Ala Ile Ala Cys Leu Tyr Val Val Leu Val Gly Glu Met Gln
 235 240 245

15
 GAG CCC ACT GTG CTG CGG CCT GCC GAC CTT GAA AAG CAG CTG TTT TCT 1243
 Glu Pro Thr Val Leu Arg Pro Ala Asp Leu Glu Lys Gln Leu Phe Ser
 250 255 260

20CTG CCA CAC TGG AGG ACA GAT GGG CAC AAC CAC GTC ATT ATC AAC CTG 1291
 Leu Pro His Trp Arg Thr Asp Gly His Asn His Val Ile Ile Asn Leu
 265 270 275

TCC CGG AAG TCA GAC ACA CAG AAT CTA CTG TAC AAC GTC AGT ACA GGC 1339
 25Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu Tyr Asn Val Ser Thr Gly
 280 285 290

CGC CAT GTG GCC CAG TCC ACC CTC TAT GCT GCC CAG TAC AGA GCT GGC 1387
 Arg His Val Ala Gln Ser Thr Leu Tyr Ala Ala Gln Tyr Arg Ala Gly
 30295 300 305 310

TTT GAC CTG GTC GTG TCA CCC CTT GTC CAT GCT ATG TCT GAA CCC AAC 1435
 Phe Asp Leu Val Val Ser Pro Leu Val His Ala Met Ser Glu Pro Asn
 315 320 325

35
 TTC ATG GAA ATC CCA CCG CAG GTG CCA GTT AAG CGG AAA TAT CTC TTC 1483
 Phe Met Glu Ile Pro Pro Gln Val Pro Val Lys Arg Lys Tyr Leu Phe
 330 335 340

40ACT TTC CAG GGC GAG AAG ATC GAG TCT CTG AGA TCT AGC CTT CAG GAG 1531
 Thr Phe Gln Gly Glu Lys Ile Glu Ser Leu Arg Ser Ser Leu Gln Glu
 345 350 355

GCC CGT TCC TTC GAG GAA GAG ATG GAG GGC GAC CCT CCG GCC GAC TAT 1579
 45Ala Arg Ser Phe Glu Glu Glu Met Glu Gly Asp Pro Pro Ala Asp Tyr
 360 365 370

GAC GAT CGC ATC ATT GCC ACC CTA AAG GCT GTA CAG GAC AGC AAG CTG 1627
 Asp Asp Arg Ile Ile Ala Thr Leu Lys Ala Val Gln Asp Ser Lys Leu
 50375 380 385 390

GAT CAG GTG CTG GTA GAA TTC ACT TGC AAA AAC CAG CCG AAG CCT AGC 1675
 Asp Gln Val Leu Val Glu Phe Thr Cys Lys Asn Gln Pro Lys Pro Ser
 395 400 405

55
 CTG CCG ACT GAG TGG GCA CTG TGT GGG GAG CGG GAA GAC CGC CTG GAG 1723
 Leu Pro Thr Glu Trp Ala Leu Cys Gly Glu Arg Glu Asp Arg Leu Glu
 410 415 420

60TTA CTG AAG CTC TCC ACC TTC GCC CTC ATC ATC ACT CCC GGG GAC CCG 1771
 Leu Leu Lys Leu Ser Thr Phe Ala Leu Ile Ile Thr Pro Gly Asp Pro
 425 430 435

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	CGC	CTG	CTC	ATT	TCA	TCT	GGG	TGT	GCC	ACG	CGG	CTC	TTC	GAG	GCC	CTG	1819
	Arg	Leu	Leu	Ile	Ser	Ser	Gly	Cys	Ala	Thr	Arg	Leu	Phe	Glu	Ala	Leu	
	440						445					450					
5	GAG	GTG	GGG	GCC	GTG	CCG	GTG	GTG	CTC	GGG	GAG	CAG	GTG	CAG	CTC	CCG	1867
	Glu	Val	Gly	Ala	Val	Pro	Val	Val	Leu	Gly	Glu	Gln	Val	Gln	Leu	Pro	
	455					460					465					470	
10	TAC	CAC	GAC	ATG	CTG	CAG	TGG	AAC	GAG	GCC	GCC	CTG	GTG	GTG	CCC	AAG	1915
	Tyr	His	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala	Ala	Leu	Val	Val	Pro	Lys	
					475					480					485		
15	CCT	CGC	GTC	ACA	GAG	GTC	CAC	TTC	CTG	TTA	CGA	AGT	CTT	TCA	GAC	AGT	1963
	Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu	Arg	Ser	Leu	Ser	Asp	Ser	
				490					495					500			
20	GAT	CTG	TTG	GCC	ATG	AGG	CGG	CAA	GGC	CGC	TTT	CTC	TGG	GAG	ACC	TAC	2011
	Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg	Phe	Leu	Trp	Glu	Thr	Tyr	
				505				510					515				
25	TTC	TCC	ACC	GCA	GAC	AGT	ATT	TTT	AAT	ACC	GTG	CTG	GCC	ATG	ATT	AGG	2059
	Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr	Val	Leu	Ala	Met	Ile	Arg	
				520			525					530					
30	ACT	CGA	ATT	CAG	ATC	CCA	GCT	GCT	CCC	ATC	CGG	GAA	GAG	GTA	GCG	GCT	2107
	Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile	Arg	Glu	Glu	Val	Ala	Ala	
						540					545					550	
35	GAG	ATC	CCC	CAT	CGT	TCA	GGC	AAA	GCA	GCT	GGA	ACT	GAC	CCC	AAC	ATG	2155
	Glu	Ile	Pro	His	Arg	Ser	Gly	Lys	Ala	Ala	Gly	Thr	Asp	Pro	Asn	Met	
					555				560						565		
40	GCT	GAC	AAT	GGG	GAC	CTG	GAC	CTG	GGG	CCG	GTA	GAG	ACA	GAA	CCA	CCC	2203
	Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Gly	Pro	Val	Glu	Thr	Glu	Pro	Pro	
				570					575					580			
45	TAT	GCC	TCA	CCT	AAA	TAC	CTC	CGC	AAT	TTC	ACT	CTG	ACT	GTC	ACA	GAC	2251
	Tyr	Ala	Ser	Pro	Lys	Tyr	Leu	Arg	Asn	Phe	Thr	Leu	Thr	Val	Thr	Asp	
				585				590					595				
50	TGT	TAC	CGT	GGC	TGG	AAC	TCT	GCC	CCG	GGA	CGG	TTC	CAT	CTT	TTT	CCC	2299
	Cys	Tyr	Arg	Gly	Trp	Asn	Ser	Ala	Pro	Gly	Arg	Phe	His	Leu	Phe	Pro	
				600			605					610					
55	CAC	ACA	CCC	TTT	GAT	CCT	GTG	TTG	CCC	TCT	GAG	GCC	AAA	TTC	TTG	GGC	2347
	His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser	Glu	Ala	Lys	Phe	Leu	Gly	
						620					625					630	
60	TCA	GGG	ACT	GGA	TTT	CGG	CCG	ATC	GGT	GGC	GGG	GCT	GGG	GGC	TCT	GGC	2395
	Ser	Gly	Thr	Gly	Phe	Arg	Pro	Ile	Gly	Gly	Gly	Ala	Gly	Gly	Ser	Gly	
					635					640					645		
65	AAG	GAG	TTC	CAG	GCA	GCG	CTC	GGA	GGC	AAT	GTC	CAG	CGG	GAG	CAG	TTC	2443
	Lys	Glu	Phe	Gln	Ala	Ala	Leu	Gly	Gly	Asn	Val	Gln	Arg	Glu	Gln	Phe	
				650					655					660			
70	ACA	GTT	GTG	ATG	CTG	ACC	TAC	GAG	CGG	GAG	GAA	GTG	CTC	ATG	AAC	TCC	2491
	Thr	Val	Val	Met	Leu	Thr	Tyr	Glu	Arg	Glu	Glu	Val	Leu	Met	Asn	Ser	
				665				670					675				
75	CTG	GAG	AGA	CTC	AAC	GGC	CTC	CCC	TAC	CTG	AAC	AAG	GTA	GTG	GTG	GTG	2539
	Leu	Glu	Arg	Leu	Asn	Gly	Leu	Pro	Tyr	Leu	Asn	Lys	Val	Val	Val	Val	
				680			685					690					

0980990-031601

[illegible]

ACTGAGGACT GTTCATAAGC CCAGGACA

3479

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly
 1 5 10 15
 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
 20 25 30
 20Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His
 35 40 45
 Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile
 25 50 55 60
 Phe Gly Pro Arg Ala Gly Ser Glu Leu Cys Glu Val Lys His Val Leu
 65 70 75 80
 30Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu
 85 90 95
 Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu
 100 105 110
 35Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu
 115 120 125
 Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu
 40 130 135 140
 Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu
 145 150 155 160
 45Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly
 165 170 175
 Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser
 180 185 190
 50Gly Phe Pro Val Tyr Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser
 195 200 205
 Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala
 55 210 215 220
 Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val
 225 230 235 240
 60Leu Val Gly Glu Met Gln Glu Pro Thr Val Leu Arg Pro Ala Asp Leu
 245 250 255
 Glu Lys Gln Leu Phe Ser Leu Pro His Trp Arg Thr Asp Gly His Asn

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 "03609920"

	260								265				270							
	His	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu				
			275					280					285							
5	Tyr	Asn	Val	Ser	Thr	Gly	Arg	His	Val	Ala	Gln	Ser	Thr	Leu	Tyr	Ala				
		290					295					300								
	Ala	Gln	Tyr	Arg	Ala	Gly	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	His				
10	305					310					315					320				
	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val				
					325					330					335					
15	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu				
				340					345					350						
	Arg	Ser	Ser	Leu	Gln	Glu	Ala	Arg	Ser	Phe	Glu	Glu	Glu	Met	Glu	Gly				
20			355					360					365							
	Asp	Pro	Pro	Ala	Asp	Tyr	Asp	Arg	Ile	Ile	Ala	Thr	Leu	Lys	Ala					
		370					375				380									
	Val	Gln	Asp	Ser	Lys	Leu	Asp	Gln	Val	Leu	Val	Glu	Phe	Thr	Cys	Lys				
25	385					390					395					400				
	Asn	Gln	Pro	Lys	Pro	Ser	Leu	Pro	Thr	Glu	Trp	Ala	Leu	Cys	Gly	Glu				
					405					410					415					
30	Arg	Glu	Asp	Arg	Leu	Glu	Leu	Leu	Lys	Leu	Ser	Thr	Phe	Ala	Leu	Ile				
				420					425					430						
	Ile	Thr	Pro	Gly	Asp	Pro	Arg	Leu	Ile	Ser	Ser	Gly	Cys	Ala	Thr					
			435				440					445								
35	Arg	Leu	Phe	Glu	Ala	Leu	Glu	Val	Gly	Ala	Val	Pro	Val	Val	Leu	Gly				
		450					455					460								
	Glu	Gln	Val	Gln	Leu	Pro	Tyr	His	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala				
40	465					470					475					480				
	Ala	Leu	Val	Val	Pro	Lys	Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu				
					485					490					495					
45	Arg	Ser	Leu	Ser	Asp	Ser	Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg				
				500					505					510						
	Phe	Leu	Trp	Glu	Thr	Tyr	Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr				
			515					520					525							
50	Val	Leu	Ala	Met	Ile	Arg	Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile				
		530					535					540								
	Arg	Glu	Glu	Val	Ala	Ala	Glu	Ile	Pro	His	Arg	Ser	Gly	Lys	Ala	Ala				
55	545					550					555					560				
	Gly	Thr	Asp	Pro	Asn	Met	Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Gly	Pro				
					565					570					575					
60	Val	Glu	Thr	Glu	Pro	Pro	Tyr	Ala	Ser	Pro	Lys	Tyr	Leu	Arg	Asn					

	595					600					605					
	Arg	Phe	His	Leu	Phe	Pro	His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser
	610					615					620					
5	Glu	Ala	Lys	Phe	Leu	Gly	Ser	Gly	Thr	Gly	Phe	Arg	Pro	Ile	Gly	Gly
	625					630					635					640
10	Gly	Ala	Gly	Gly	Ser	Gly	Lys	Glu	Phe	Gln	Ala	Ala	Leu	Gly	Gly	Asn
					645					650				655		
	Val	Gln	Arg	Glu	Gln	Phe	Thr	Val	Val	Met	Leu	Thr	Tyr	Glu	Arg	Glu
				660					665					670		
15	Glu	Val	Leu	Met	Asn	Ser	Leu	Glu	Arg	Leu	Asn	Gly	Leu	Pro	Tyr	Leu
			675					680					685			
	Asn	Lys	Val	Val	Val	Val	Trp	Asn	Ser	Pro	Lys	Leu	Pro	Ser	Glu	Asp
	690					695					700					
20	Leu	Leu	Trp	Pro	Asp	Ile	Gly	Val	Pro	Ile	Met	Val	Val	Arg	Thr	Glu
	705					710					715					720
	Lys	Asn	Ser	Leu	Asn	Asn	Arg	Phe	Leu	Pro	Trp	Asn	Glu	Ile	Glu	Thr
25					725					730					735	
	Glu	Ala	Ile	Leu	Ser	Ile	Asp	Asp	Asp	Ala	His	Leu	Arg	His	Asp	Glu
				740				745						750		
30	Ile	Met	Phe	Gly	Phe	Trp	Val	Trp	Arg	Glu	Ala	Arg	Asp	Arg	Ile	Val
			755					760					765			
	Gly	Phe	Pro	Gly	Arg	Tyr	His	Ala	Trp	Asp	Ile	Pro	His	Gln	Ser	Trp
	770					775					780					
35	Leu	Tyr	Asn	Ser	Asn	Tyr	Ser	Cys	Glu	Leu	Ser	Met	Val	Leu	Thr	Gly
	785					790					795					800
	Ala	Ala	Phe	Phe	His	Lys	Tyr	Tyr	Ala	Tyr	Leu	Tyr	Ser	Tyr	Val	Met
40					805					810					815	
	Pro	Gln	Ala	Ile	Arg	Asp	Met	Val	Asp	Glu	Tyr	Ile	Asn	Cys	Glu	Asp
				820					825					830		
45	Ile	Ala	Met	Asn	Phe	Leu	Val	Ser	His	Ile	Thr	Arg	Lys	Pro	Pro	Ile
			835					840					845			
	Lys	Val	Thr	Ser	Arg	Trp	Thr	Phe	Arg	Cys	Pro	Gly	Cys	Pro	Gln	Ala
	850					855					860					
50	Leu	Ser	His	Asp	Asp	Ser	His	Phe	His	Glu	Arg	His	Lys	Cys	Ile	Asn
	865					870					875					880
	Phe	Phe	Val	Lys	Val	Tyr	Gly	Tyr	Met	Pro	Leu	Leu	Tyr	Thr	Gln	Phe
55					885					890					895	
	Arg	Val	Asp	Ser	Val	Leu	Phe	Lys	Thr	Arg	Leu	Pro	His	Asp	Lys	Thr
				900					905					910		
60	Lys	Cys	Phe	Lys	Phe	Ile										
				915												

(2) INFORMATION FOR SEQ ID NO:3:

5

(11) MOLECULE TYPE: DNA (genomic)

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10      (ix) FEATURE:
           (A) NAME/KEY: CDS
           (B) LOCATION: 594..3350

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15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	GGCGGGTCCC	TGAGCTGGAA	GCCGGAGAGC	AAGCCCTGGA	GGTTCACTCT	TTCAAGAAGT	60
20	CGTGTGCTGA	GGTGTAAATGC	TACACAAGTC	AGAGGAAGGA	AGGGTCCTGA	AACACATGGC	120
	CTGATTGTTG	GCAAAGGCAT	CATAAGAAGC	TGGCATTAT	TTCTGTTCTA	ACCTATTACT	180
	GTATAACTGT	GAATAGACAC	TATGCATATT	TGTTGGTCAG	CAAAACCAAG	AAACAAGAGC	240
25	TATGGCATT	GAAAAAGTCT	GTCTGATTCC	AGGGTGT	TTTTCCTGGGTTT	CATCATCAGG	300
	TACCTCCTCC	CTTTCATCTC	AGCAAGAATG	TGGCACCTTT	TATCGTTTGA	TAAAGATTAA	360
30	GGACATGTT	TTTGGTCAAC	AGCCAGAACT	TAAAATCTGC	TGGAATAGGG	TCAGAGACCA	420
	TTTCAGCTGC	AGCTGAGGAA	AATGAAATGT	TCATTTTATT	TGGTGCCTTG	TCTGGGGAGC	480
	ACACTAACTC	TTCTGGAAAC	GTGTCACTGA	AACAGAGATC	GTTTTGTGGA	ATAGCAACCC	540
35	ATGGTTATGG	CGAGTGACCC	GACGTGATCT	GGGGGGCAGG	CTGCAGAGGA	CTC ATG	596
						Met	

ACA GGC TAT ACC ATG CTG CGG AAT GGG GGC GCG GGG AAC GGA GGT CAG 644
40Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Ala Gly Asn Gly Gly Gln
920 925 930 935

ACC TGC ATG CTG CGC TGG TCC AAC CGC ATC CGC CTC ACG TGG CTC AGC 692
Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser
45 940 945 950

TTC ACG CTC TTT GTC ATC CTG GTC TTC TTC CCG CTC ATC GCC CAC TAT 740
Phe Thr Leu Phe Val Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr
955 960 965

50

TAC	CTC	ACC	ACT	CTG	GAT	GAG	GCT	GAT	GAG	GCA	GGC	AAG	CGG	ATT	TTT	788
Tyr	Leu	Thr	Thr	Leu	Asp	Glu	Ala	Asp	Glu	Ala	Gly	Lys	Arg	Ile	Phe	
		970					975					980				

55GGT CCC CGG GTG GGG AAC GAG CTG TGC GAG GTG AAG CAC GTG CTG GAT 836
Gly Pro Arg Val Gly Asn Glu Leu Cys Glu Val Lys His Val Leu Asp
985 990 995

CTG TGC CGC ATC CGG GAG TCG GTG AGT GAA GAG CTC CTG CAG CTG GAG 884
60Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu
1000 1005 1010 1015

GCC AAG CGC CAA GAG CTG AAC AGC GAG ATC GCC AAG CTG AAT CTG AAG 932

	Ala	Lys	Arg	Gln	Glu	Leu	Asn	Ser	Glu	Ile	Ala	Lys	Leu	Asn	Leu	Lys	
					1020					1025					1030		
	ATC	GAA	GCC	TGT	AAG	AAG	AGC	ATT	GAG	AAC	GCC	AAG	CAG	GAC	CTG	CTC	980
5	Ile	Glu	Ala	Cys	Lys	Lys	Ser	Ile	Glu	Asn	Ala	Lys	Gln	Asp	Leu	Leu	
				1035					1040					1045			
	CAG	CTC	AAG	AAT	GTC	ATC	AGC	CAG	ACC	GAG	CAT	TCC	TAC	AAG	GAG	CTC	1028
10	Gln	Leu	Lys	Asn	Val	Ile	Ser	Gln	Thr	Glu	His	Ser	Tyr	Lys	Glu	Leu	
			1050					1055					1060				
	ATG	GCC	CAG	AAC	CAG	CCC	AAG	CTG	TCC	CTG	CCC	ATC	CGA	CTG	CTC	CCA	1076
	Met	Ala	Gln	Asn	Gln	Pro	Lys	Leu	Ser	Leu	Pro	Ile	Arg	Leu	Leu	Pro	
		1065					1070					1075					
15	GAG	AAG	GAC	GAT	GCC	GGC	CTC	CCT	CCC	CCG	AAG	GCC	ACT	CGG	GGC	TGC	1124
	Glu	Lys	Asp	Asp	Ala	Gly	Leu	Pro	Pro	Pro	Lys	Ala	Thr	Arg	Gly	Cys	
	1080					1085					1090					1095	
20	CGG	CTA	CAC	AAC	TGC	TTT	GAT	TAT	TCT	CGT	TGC	CCT	CTC	ACC	TCT	GGC	1172
	Arg	Leu	His	Asn	Cys	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser	Gly	
				1100						1105					1110		
	TTC	CCG	GTC	TAC	GTC	TAT	GAC	AGT	GAC	CAG	TTT	GTC	TTT	GGC	AGC	TAC	1220
25	Phe	Pro	Val	Tyr	Val	Tyr	Asp	Ser	Asp	Gln	Phe	Val	Phe	Gly	Ser	Tyr	
				1115					1120					1125			
	CTG	GAT	CCC	TTG	GTC	AAG	CAG	GCT	TTT	CAG	GCG	ACA	GCA	CGA	GCT	AAC	1268
30	Leu	Asp	Pro	Leu	Val	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Ala	Arg	Ala	Asn	
			1130					1135					1140				
	GTT	TAT	GTT	ACA	GAA	AAT	GCA	GAC	ATC	GCC	TGC	CTT	TAC	GTG	ATA	CTA	1316
	Val	Tyr	Val	Thr	Glu	Asn	Ala	Asp	Ile	Ala	Cys	Leu	Tyr	Val	Ile	Leu	
		1145					1150					1155					
35	GTG	GGA	GAG	ATG	CAG	GAG	CCC	GTG	GTG	CTG	CGG	CCT	GCT	GAG	CTG	GAG	1364
	Val	Gly	Glu	Met	Gln	Glu	Pro	Val	Val	Leu	Arg	Pro	Ala	Glu	Leu	Glu	
	1160					1165					1170				1175		
40	AAG	CAG	TTG	TAT	TCC	CTG	CCA	CAC	TGG	CGG	ACG	GAT	GGA	CAC	AAC	CAT	1412
	Lys	Gln	Leu	Tyr	Ser	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn	His	
				1180					1185					1190			
	GTC	ATC	ATC	AAT	CTG	TCA	CGT	AAG	TCA	GAT	ACA	CAG	AAC	CTT	CTC	TAT	1460
45	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu	Tyr	
				1195					1200					1205			
	AAC	GTC	AGT	ACT	GGC	CGT	GCC	ATG	GTG	GCC	CAG	TCC	ACC	TTC	TAC	ACT	1508
50	Asn	Val	Ser	Thr	Gly	Arg	Ala	Met	Val	Ala	Gln	Ser	Thr	Phe	Tyr	Thr	
			1210					1215					1220				
	GTC	CAG	TAC	AGA	CCT	GGC	TTT	GAC	TTG	GTC	GTA	TCA	CCG	CTG	GTC	CAT	1556
	Val	Gln	Tyr	Arg	Pro	Gly	Phe	Asp	Leu	Val	Val		1235				
		1225					1230										
55	GCC	ATG	TCT	GAG	CCC	AAC	TTC	ATG	GAA	ATC	CCA	CCA	CAG	GTG	CCG	GTG	1604
	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val	
	1240					1245					1250				1255		
60	AAG	CGG	AAA	TAT	CTC	TTC	ACC	TTC	CAG	GGC	GAG	AAG	ATT	GAG	TCT	CTG	1652
	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu	
				1260						1265				1270			

	AGG	TCT	AGC	CTT	CAG	GAG	GCC	CGC	TCC	TTC	GAA	GAG	GAA	ATG	GAG	GGC	1700
	Arg	Ser	Ser	Leu	Gln	Glu	Ala	Arg	Ser	Phe	Glu	Glu	Glu	Met	Glu	Gly	
				1275					1280					1285			
5	GAC	CCT	CCC	GCC	GAC	TAC	GAT	GAC	CGG	ATC	ATT	GCC	ACC	CTG	AAG	GCG	1748
	Asp	Pro	Pro	Ala	Asp	Tyr	Asp	Asp	Arg	Ile	Ile	Ala	Thr	Leu	Lys	Ala	
				1290					1295					1300			
	GTG	CAG	GAC	AGC	AAG	CTG	GAT	CAG	GTC	CTG	GTG	GAA	TTC	ACC	TGC	AAA	1796
10	Val	Gln	Asp	Ser	Lys	Leu	Asp	Gln	Val	Leu	Val	Glu	Phe	Thr	Cys	Lys	
								1310					1315				
	AAC	CAG	CCC	AAA	CCC	AGC	CTG	CCG	ACT	GAG	TGG	GCA	CTG	TGT	GGA	GAG	1844
	Asn	Gln	Pro	Lys	Pro	Ser	Leu	Pro	Thr	Glu	Trp	Ala	Leu	Cys	Gly	Glu	
15	1320						1325				1330					1335	
	CGG	GAG	GAC	CGC	TTG	GAA	TTG	CTG	AAG	CTC	TCC	ACC	TTC	GCC	CTC	ATC	1892
	Arg	Glu	Asp	Arg	Leu	Glu	Leu	Leu	Lys	Leu	Ser	Thr	Phe	Ala	Leu	Ile	
					1340						1345					1350	
20																	
	ATT	ACC	CCC	GGG	GAC	CCT	CGC	TTG	GTT	ATT	TCC	TCT	GGG	TGT	GCA	ACA	1940
	Ile	Thr	Pro	Gly	Asp	Pro	Arg	Leu	Val	Ile	Ser	Ser	Gly	Cys	Ala	Thr	
					1355					1360					1365		
25	CGG	CTC	TTC	GAA	GCC	CTG	GAA	GTC	GGT	GCC	GTC	CCG	GTG	GTG	CTG	GGG	1988
	Arg	Leu	Phe	Glu	Ala	Leu	Glu	Val	Gly	Ala	Val	Pro	Val	Val	Leu	Gly	
					1370				1375					1380			
	GAG	CAG	GTC	CAG	CTT	CCC	TAC	CAG	GAC	ATG	CTG	CAG	TGG	AAC	GAG	GCG	2036
30	Glu	Gln	Val	Gln	Leu	Pro	Tyr	Gln	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala	
								1390					1395				
	GCC	CTG	GTG	GTG	CCA	AAG	CCT	CGT	GTT	ACC	GAG	GTT	CAT	TTC	CTG	CTC	2084
	Ala	Leu	Val	Val	Pro	Lys	Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu	
35	1400						1405					1410				1415	
	AGA	AGC	CTC	TCC	GAT	AGT	GAC	CTC	CTG	GCT	ATG	AGG	CGG	CAA	GGC	CGC	2132
	Arg	Ser	Leu	Ser	Asp	Ser	Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg	
						1420					1425					1430	
40																	
	TTT	CTC	TGG	GAG	ACT	TAC	TTC	TCC	ACT	GCT	GAC	AGT	ATT	TTT	AAT	ACC	2180
	Phe	Leu	Trp	Glu	Thr	Tyr	Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr	
					1435					1440					1445		
45	GTG	CTG	GCT	ATG	ATT	AGG	ACT	CGC	ATC	CAG	ATC	CCA	GCC	GCT	CCC	ATC	2228
	Val	Leu	Ala	Met	Ile	Arg	Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile	
					1450				1455								

	CCT	TTC	CAT	CTT	TTC	CCC	CAC	ACT	CCC	TTT	GAC	CCT	GTG	TTG	CCC	TCA	2468
	Pro	Phe	His	Leu	Phe	Pro	His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser	
			1530					1535					1540				
5	GAG	GCC	AAA	TTC	TTG	GGC	TCA	GGG	ACT	GGC	TTT	CGG	CCT	ATT	GGT	GGT	2516
	Glu	Ala	Lys	Phe	Leu	Gly	Ser	Gly	Thr	Gly	Phe	Arg	Pro	Ile	Gly	Gly	
		1545					1550					1555					
10	GGA	GCT	GGG	GGT	TCT	GGC	AAG	GAA	TTT	CAG	GCA	GCG	CTT	GGA	GGC	AAT	2564
	Gly	Ala	Gly	Gly	Ser	Gly	Lys	Glu	Phe	Gln	Ala	Ala	Leu	Gly	Gly	Asn	
		1560					1565				1570					1575	
15	GTT	CCC	CGA	GAG	CAG	TTC	ACG	GTG	GTG	ATG	TTG	ACT	TAT	GAG	CGG	GAG	2612
	Val	Pro	Arg	Glu	Gln	Phe	Thr	Val	Val	Met	Leu	Thr	Tyr	Glu	Arg	Glu	
					1580					1585					1590		
20	GAA	GTG	CTT	ATG	AAC	TCT	TTA	GAG	AGG	CTG	AAT	GGC	CTC	CCT	TAC	CTG	2660
	Glu	Val	Leu	Met	Asn	Ser	Leu	Glu	Arg	Leu	Asn	Gly	Leu	Pro	Tyr	Leu	
				1595					1600					1605			
25	AAC	AAG	GTC	GTG	GTG	GTG	TGG	AAT	TCT	CCC	AAG	CTG	CCA	TCA	GAG	GAC	2708
	Asn	Lys	Val	Val	Val	Val	Trp	Asn	Ser	Pro	Lys	Leu	Pro	Ser	Glu	Asp	
		--	1610					1615					1620				
30	CTT	CTG	TGG	CCT	GAC	ATT	GGC	GTT	CCC	ATC	ATG	GTG	GTC	CGT	ACT	GAG	2756
	Leu	Leu	Trp	Pro	Asp	Ile	Gly	Val	Pro	Ile	Met	Val	Val	Arg	Thr	Glu	
		1625					1630					1635					
35	AAG	AAC	AGT	TTG	AAC	AAC	CGA	TTC	TTA	CCC	TGG	AAT	GAA	ATT	GAG	ACA	2804
	Lys	Asn	Ser	Leu	Asn	Asn	Arg	Phe	Leu	Pro	Trp	Asn	Glu	Ile	Glu	Thr	
		1640				1645					1650					1655	
40	GAG	GCC	ATC	CTG	TCC	ATT	GAT	GAC	GAT	GCT	CAC	CTC	CGC	CAT	GAC	GAA	2852
	Glu	Ala	Ile	Leu	Ser	Ile	Asp	Asp	Asp	Ala	His	Leu	Arg	His	Asp	Glu	
				1660						1665					1670		
45	ATC	ATG	TTT	GGG	TTC	CGG	GTG	TGG	AGA	GAA	GCT	CGG	GAC	CGC	ATC	GTG	2900
	Ile	Met	Phe	Gly	Phe	Arg	Val	Trp	Arg	Glu	Ala	Arg	Asp	Arg	Ile	Val	
				1675				1680						1685			
50	GGC	TTC	CCT	GGC	CGT	TAC	CAC	GCA	TGG	GAC	ATC	CCC	CAT	CAG	TCC	TGG	2948
	Gly	Phe	Pro	Gly	Arg	Tyr	His	Ala	Trp	Asp	Ile	Pro	His	Gln	Ser	Trp	
		1690					1695						1700				
55	CTC	TAC	AAC	TCC	AAC	TAC	TCC	TGT	GAG	CTG	TCC	ATG	GTG	CTG	ACA	GGT	2996
	Leu	Tyr	Asn	Ser	Asn	Tyr	Ser	Cys	Glu	Leu	Ser	Met	Val	Leu	Thr	Gly	
		1705					1710					1715					
60	GCT	GCC	TTT	TTT	CAC	AAG	TAT	TAT	GCC	TAC	CTG	TAT	TCT	TAT	GTG	ATG	3044
	Ala	Ala	Phe	Phe	His	Lys	Tyr	Tyr	Ala	Tyr	Leu	Tyr	Ser	Tyr	Val	Met	
		1720				1725					1730					1735	
65	CCC	CAG	GCC	ATC	CGG	GAC	ATG	GTG	GAT	GAA	TAC	ATC	AAC	TGT	GAG	GAC	3092
	Pro	Gln	Ala	Ile	Arg	Asp	Met	Val	Asp	Glu	Tyr	Ile	Asn	Cys	Glu	Asp	
				1740						1745					1750		
70	ATT	GCC	ATG	AAC	TTC	CTT	GTC	TCC	CAC	ATC	ACT	CGG	AAG	CCC	CCC	ATC	3140
	Ile	Ala	Met	Asn	Phe	Leu	Val	Ser	His	Ile	Thr	Arg	Lys	Pro	Pro	Ile	
				1755					1760					1765			
75	AAG	GTG	ACC	TCA	CGG	TGG	ACA	TTC	CGA	TGC	CCA	GGA	TGC	CCT	CAG	GCC	3188
	Lys	Val	Thr	Ser	Arg	Trp	Thr	Phe	Arg	Cys	Pro	Gly	Cys	Pro	Gln	Ala	
		1770						1775					1780				

	CTG TCT CAT GAT GAC TCC CAC TTC CAC GAG CGG CAC AAG TGC ATC AAC	3236
	Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn	
	1785 1790 1795	
5	TTC TTC GTG AAG GTG TAC GGC TAC ATG CCC CTC CTG TAC ACG CAG TTC	3284
	Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe	
	1800 1805 1810 1815	
10	AGG GTG GAT TCT GTG CTC TTC AAG ACA CGC CTG CCC CAT GAC AAG ACC	3332
	Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr	
	1820 1825 1830	
15	AAG TGC TTC AAG TTC ATC TAGGGGCAGC GCACGGTCTG GGGAAGAGGA	3380
	Lys Cys Phe Lys Phe Ile	
	1835	
	TGAGCAGAGG GAGGAAGATG GCTCCCAAGG TTCCTAGGCA TTGCAGGACC TTGGGCACAT	3440
	CTGCTGGTGG GTGGCCCAGA GCCTCTGCTG GAAGGGGCAG CAGGAGGAGT GGAAGGAAAC	3500
20	CGCTGCCTTT ATCTTGAAGT CAGCCACACT GGGCCTGGAG CCCTGGGCGG AGTCCCCGGG	3560
	GTTCCCCACA CAGGGCACTG ACTGATAGCT TACACTGAGG ACTGTGGCGA CTCTGCAGAG	3620
25	TCACTCACAC CGTTCGTACG CCCAGGACAG CTGGTTCGTG GTTTTTACAT TCAATAACAA	3680
	CTATTATGAT TATTTAAAAA GAGAAAGTTT CAGATTTGCC ATTCAAGGCT TATTTATATA	3740
	TATGTGTGTG TATATAAATA CATGCACACA CTGCATACA TATATATTTT TGGCTGGGGG	3800
30	AGTGTGAGTT TTGCCTTTCT AAGGGAGGGA CCGCGCAGGC TCCTTTGTTC TGTATTCTGG	3860
	CGGAGATGGG TCCTGGCCTT GTGTCACCTG CTTATCCTTA AAGATCATCT CCCATCCTCC	3920
35	CCAGCGCCAT CTGTGTGCAG CAACCAGAAA GGGATGAAC TGGCCCTCTT GCGGGCCTGG	3980
	ACAAGGTCTC TTCCTTACCC TTTCTGTTGC CAGTCAGCAA CCTGTAACTC ACATTCTCTT	4040
	CCCAGTGAAT CCCTGGGAGC GCCTGACCCT GGTGGGCTGT TCAGCTTCCT GCTGCTGGGG	4100
40	CCAGCGATTT TTGAGGATTT ATCTTTAGGC CAGGCTTGCC TCCGTACTTA TCCCTGCTCT	4160
	CCCATTCTC TCTTGTGTTGA GAGAGAATGA GGAAGCAAAG AGTGAGAAAG AATAGGGGCT	4220
45	GAAGACGCCA CTCCCAGATG GCTCTTTCTA TCCTGCTCTT CTGTTGAAAC ACACGTGCTG	4280
	TGGGCCTCAG GCGTTTCTGA AGTGCTCTTT CTTGGATTGG ACAGGAGATC AGCAGCGTGC	4340
	ACATCTGCTG TGGTCTGAAG TGGTTTGCAG GTCAGCCTCC TCTCCCTAGT GTAGAGCAAG	4400
50	CCAGTGCCT TCGAGGAACC CACCCGGCTG GCCGGGAAGT TTTACAGCAA GGCGCCTGCC	4460
	TTGGGATAAT TCCTTGGTGA AATTCACCTT CCCCCGCCT CTGTCTGGAG CCCCATCCTG	4520
55	TGTTATCTGT GGTTTTTTGA CCCCTAATGT CAGCTTGGCT GTAGGACTCC CCGAGGTTTG	4580
	GTATGTGCTA GAACAATGGG AGGCTGTGAT TTGCTGTGTA AGCTCACATC CAGCCTTGGA	4640
	ATCTAACGGG CATTACAAAC CCGAGTTACC ACTTCCACT CCCTGCTTAG GATTCTGTTC	4700
60	CCTGGGCTGA AACTGAAATA AGCTAATTTT TTGGGTCACG GTGGCAGTAG GGGAACCTAG	4760
	GAGGGTGTGA GTGGCATTG TCAGGGATTT AGCCCATGAC GTGTTTCTTG AACCCTACTT	4820

TCTGGAAGTG GAGTTGACTC TGGAAGTTTT CTAGCAACTG AACAAAAGCT CAGGTTTGTC 4880
 CTGGTCATGC ACATGCCTTA AGCCAGTTCC GTCTTCCCTA GACCTTGGCA TCCTGTGCTT 4940
 5CTATTTCTTG GAATACGTTT TCCTCTGACC TGCCTGTACC ACGTGGGTCC TCTTCAAGTA 5000
 CTGTTTTGAA GCTGGGCTCT TTTGTGTAGC TCCCACCCAC CTGTAGGGCT AGCTCGGCTT 5060
 AAGGGAACTC TCCCCATTGG CAAACCGGAC CCGGCCGCCG CCAGGACTGT GTTTCCAAAG 5120
 10 GTTCCCCGCC CCCAACCCCA GCATCAGCCT GTAGCTCCCC TGCTGAGGCA GTGTGGTTAT 5180
 GTTCCCAGCA GTGGGGGTCA GACGCCCTTC CTCAGAACTT TCTAGTTGCC CTCTACCTGA 5240
 15CTCCTGACTT GTATTCTTTT TAGCAGTAGC CTTCTTCCCT CGGGGAGCCA AAGAGTGTGG 5300
 TGTGTGGCGC TATATTGTGG CTGCTATTTT ATCTGGTTTC TTTTAATGTG AGGAACTCAC 5360
 ATRACTGACTT CAGTGGGACT CGGTGAGCCG GGGCCGTCTG TGTGGTGGGA CCCCCTTTAG 5420
 20 CGGGACTCAG TGAGCTGGGG CCGTCTGTGT GGTGGAGCCA GGGCCTCTCC CTTTAGTGGA 5480
 GCCAGGTTGT CGGGCCCCGA ATGTCACTGG TGGATCTAAG AAGGGCTGAG TGGTCTGACA 5540
 25CCAAAACATG CCGCAGGGAG GGCTGTGGTG CCGGTGCTTC CAACAAGGAC AGCCCTCCTT 5600
 GACCCTGAAA GGAACACTGG CTTGAAGGAC TGCAGACAGG CTCTGAGGGG CACGCCCTCC 5660
 TCAGCGAGAG GCAGCAAGGT GGCCACAGTG TCACTGGTCA GGTGCTTCTC ACCACGGGAA 5720
 30 AGCCGCCGAC CTGTGACTCG CTTGAGATGG GAAAGCGGCG CCACAGACCC CGGGTCTCCT 5780
 TGGCTGTCTG TGGGCCGCCC CTGGCCACCT TGTCTGGCT CGCAGGGTGC AGGAGCGCCT 5840
 35CGTTCTCTGG GTGGCCGGCT TGCTGCTCCG GTTTGGGCTG TCTTACCATA ACACCGTCCC 5900
 AGGGCTCTGC AGGCCACTGT GAGCGCTGGC TCCCTGGGCA GTGCTCCTCC GTGTGGACTG 5960
 TGCCTCAGGC CAGGGCTCAC CAGCTGGGGT CCTGTCCGGA AGGATGGGAT CTTTCTGGGA 6020
 40 GCTGCGCCGG ACAGAGTGGG GAGCTCCTAG TTTGTGGGGG GAAGCTTTGA TATCCATGCC 6080
 ACGTCCATCC ACCCCACCCC TTTTCGTCAC GAGCACAATG GTCTTACATT GGATTTTTGT 6140
 45AAAAAATAA AAATAAATGG AGACTTTAAC TC 6172

(2) INFORMATION FOR SEQ ID NO:4:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 919 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Ala Gly Asn Gly Gly
 60 1 5 10 15
 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
 20 25 30

60 Phe Ala Leu Ile Ile Thr Pro Gly Asp Pro Arg Leu Val Ile Ser Ser
20 25 30

Gly Cys Ala Thr Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro
 35 40 45
 5 Val Val Leu Gly Glu Gln Val Gln Leu Pro Tyr Gln Asp Met Leu Gln
 50 55 60
 Trp Asn Glu Ala Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val
 65 70 75 80
 10 His Phe Leu Leu Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg
 85 90 95
 Arg Gln Gly Arg Phe Leu Trp Glu Thr Tyr Phe Pro Thr Ala Asp Ser
 100 105 110
 15 Ile Phe Asn Thr Val Leu Ala Met Ile Arg Thr Arg Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 Arg Cys His Lys His Gln Val Phe Asp Tyr Pro Gln Val Leu Gln Glu
 1 5 10 15
 Ala Thr Phe Cys Val Val Leu Arg Gly Ala Arg Leu Gly Gln Ala Val
 20 25 30
 40 Leu Ser Asp Val Leu Gln Ala Gly Cys Val Pro Val Val Ile Ala Asp
 35 40 45
 Ser Tyr Ile Leu Pro Phe Ser Glu Val Leu Asp Trp Lys Arg Ala Ser
 50 55 60
 45 Val Val Val Pro Glu Glu Lys Met Ser Asp Val Tyr Ser Ile Leu Gln
 65 70 75 80
 50 Ser Ile Pro Gln Arg Gln Ile Glu Glu Met Gln Arg Gln Ala Arg Trp
 85 90 95
 Phe Trp Glu Ala Tyr Phe Gln Ser Ile Lys Ala Ile Ala Leu Ala Thr
 100 105 110
 55 Leu Gln Ile Ile Asn Asp Arg Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:7:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

TESTED: 02550860

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10	Arg 1	Cys	Asp	Arg	Asp 5	Asn	Thr	Glu	Tyr	Glu 10	Lys	Tyr	Asp	Tyr	Arg 15	Glu
	Met	Leu	His	Asn 20	Ala	Thr	Phe	Cys	Leu 25	Val	Pro	Arg	Gly	Arg 30	Arg	Leu
15	Gly	Ser	Phe 35	Arg	Phe	Leu	Glu	Ala 40	Leu	Gln	Ala	Ala	Cys 45	Val	Pro	Val
	Met	Leu 50	Ser	Asn	Gly	Trp	Glu 55	Leu	Pro	Phe	Ser	Glu 60	Val	Ile	Asn	Trp
20	Asn 65	Gln	Ala	Ala	Val	Ile 70	Gly	Asp	Glu	Arg	Leu 75	Leu	Leu	Gln	Ile	Pro 80
	Ser	Thr	Ile	Arg	Ser 85	Ile	His	Gln	Asp	Lys 90	Ile	Leu	Ala	Leu	Arg 95	Gln
25	Gln	Thr	Gln	Phe 100	Leu	Trp	Glu	Ala	Tyr 105	Phe	Ser	Ser	Val	Glu 110	Lys	Ile
30	Val	Leu	Thr 115	Thr	Leu	Glu	Ile	Ile 120	Gln	Asp	Arg	Ile				

(2) INFORMATION FOR SEQ ID NO:8:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50	Arg 1	Cys	Glu	Gln	Asp 5	Pro	Gly	Pro	Gly	Gln 10	Thr	Gln	Arg	Gln	Glu 15	Thr
	Leu	Pro	Asn 20	Ala	Thr	Phe	Cys	Leu	Ile 25	Ser	Gly	His	Arg	Pro 30	Glu	Ala
55	Ala	Ser	Arg 35	Phe	Leu	Gln	Ala	Leu 40	Gln	Ala	Gly	Cys	Ile 45	Pro	Val	Leu
	Leu	Ser 50	Pro	Arg	Trp	Glu	Leu 55	Pro	Phe	Ser	Glu	Val 60	Ile	Asp	Trp	Thr
60	Lys 65	Ala	Ala	Ile	Val	Ala 70	Asp	Glu	Arg	Leu	Pro 75	Leu	Gln	Val	Leu	Ala 80

Ala Leu Gln Glu Met Ser Pro Ala Arg Val Leu Ala Leu Arg Gln Gln
 85 90 95
 5 Thr Gln Phe Leu Trp Asp Ala Tyr Phe Ser Ser Val Glu Lys Val Ile
 100 105 110
 His Thr Thr Leu Glu Val Ile Gln Asp Arg Ile
 115 120

10(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25 Lys Cys Ser Gln Glu Asn Cys Ser Leu Glu Arg Arg Arg Gln Leu Ile
 1 5 10 15
 Gly Ser Ser Thr Phe Cys Phe Leu Leu Pro Ser Glu Met Phe Phe Gln
 20 25 30
 30 Asp Phe Leu Ser Ser Leu Gln Leu Gly Cys Ile Pro Ile Leu Leu Ser
 35 40 45
 35 Asn Ser Gln Leu Leu Pro Phe Gln Asp Leu Ile Asp Trp Arg Arg Ala
 50 55 60
 Thr Tyr Arg Leu Pro Leu Ala Arg Leu Pro Glu Ala His Phe Ile Val
 65 70 75 80
 40 Gln Ser Phe Glu Ile Ser Asp Ile Ile Glu Met Arg Arg Val Gly Arg
 85 90 95
 Leu Phe Tyr Glu Thr Tyr Leu Ala Asp Arg His Leu Leu Ala Arg Ser
 100 105 110
 45 Leu Leu Ala Ala Leu Arg Tyr Lys Leu
 115 120

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

(2) INFORMATION FOR SEQ ID NO:11:

60 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Pro Gln Ser Gln Gly Phe Thr Gln Ile Val Leu Thr Tyr Asp Arg Val
 1 5 10 15
 Glu Ser Leu Phe Arg Val Ile Thr Glu Val Ser Lys Val Pro Ser Leu
 20 25 30
 10 Ser Lys Leu Leu Val Val Trp Asn Asn Gln Asn Lys Asn Pro Pro Glu
 35 40 45
 Asp Ser Leu Trp Pro Lys Ile Arg Val Pro Leu Lys Val Val Arg Thr
 50 55 60
 15 Ala Glu Asn Lys Leu Ser Asn Arg Phe Phe Pro Tyr Asp Glu Ile Glu
 65 70 75 80
 Thr Glu Ala Val Leu Ala Ile Asp Asp Asp Ile Ile Met Leu Thr Ser
 85 90 95
 20 Asp Glu Leu Gln Phe Gly Tyr Glu Val Trp Arg Glu Phe Pro Asp Arg
 100 105 110
 25 Leu Val Gly Tyr Pro Gly Arg Leu His Leu Trp Asp His Glu Ala Met
 115 120 125
 Asn Lys Trp Lys Tyr Glu Ser Glu Trp Thr Asn Glu Val Ser Met Val
 130 135 140
 30 Leu Thr Gly Ala Ala Phe Tyr His Lys Tyr Phe Asn Tyr Leu Tyr Thr
 145 150 155 160
 Lys Met Pro Gly Asp Ile Lys Asn Trp Val Asp Ala His Met Asn Cys
 165 170 175
 35 Tyr Glu Asp Ile Ala Met Asn Phe Leu Val Ala Asn Val Thr Gly Lys
 180 185 190
 40 Ala Val Ile Lys Val Thr Pro Arg Lys Lys Phe Lys Cys Pro Glu Cys
 195 200 205
 Thr Ala Ile Asp Gly Leu Ser Leu Asp Gln Thr His Met Val Glu Arg
 210 215 220
 45 Ser Glu Cys Ile Asn Lys Phe Ala Ser Val Phe Gly Thr Met Pro Leu
 225 230 235 240
 Lys Val Val Glu His Arg Ala Asp Pro Val Leu Tyr Lys Asp Asp Phe
 245 250 255
 50 Pro Glu Lys Leu Lys Ser Phe Pro Asn Ile Gly Ser Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:12:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5	Pro 1	Pro	Ser	Lys	Phe 5	Thr	Ala	Val	Ile	His 10	Ala	Val	Thr	Pro	Leu	Val
	Ser	Gln	Ser	Gln 20	Pro	Val	Leu	Lys	Leu 25	Leu	Val	Ala	Ala	Ala 30	Lys	Ser
10	Gln	Tyr	Cys 35	Ala	Gln	Ile	Ile	Val 40	Leu	Trp	Asn	Cys	Asp 45	Lys	Pro	Leu
	Pro 50	Ala	Lys	His	Arg	Trp	Pro 55	Ala	Thr	Ala	Val	Pro 60	Val	Val	Val	Ile
15	Glu 65	Gly	Glu	Ser	Lys	Val 70	Met	Ser	Ser	Arg	Phe 75	Leu	Pro	Tyr	Asp	Asn 80
20	Ile	Ile	Thr	Asp 85	Ala	Val	Leu	Ser	Leu 90	Asp	Glu	Asp	Thr	Val	Leu 95	Ser
	Thr	Thr	Glu	Val 100	Asp	Phe	Ala	Phe	Thr 105	Val	Trp	Gln	Ser	Phe 110	Pro	Glu
25	Arg	Ile	Val 115	Gly	Tyr	Pro	Ala	Arg 120	Ser	His	Phe	Trp	Asp 125	Asn	Ser	Lys
	Glu 130	Arg	Trp	Gly	Tyr	Thr	Ser 135	Lys	Trp	Thr	Asn	Asp 140	Tyr	Ser	Met	Val
30	Leu 145	Thr	Gly	Ala	Ala	Ile 150	Tyr	His	Lys	Tyr	Tyr 155	His	Tyr	Leu	Tyr	Ser 160
35	His	Tyr	Leu	Pro 165	Ala	Ser	Leu	Lys	Asn 170	Met	Val	Asp	Gln	Leu 175	Ala	Asn
	Cys	Glu	Asp 180	Ile	Leu	Met	Asn	Phe 185	Leu	Val	Ser	Ala	Val	Thr 190	Lys	Leu
40	Pro	Pro 195	Ile	Lys	Val	Thr	Gln 200	Lys	Lys	Gln	Tyr	Lys 205	Glu	Thr	Met	Met
	Gly 210	Gln	Thr	Ser	Arg	Ala	Ser 215	Arg	Trp	Ala	Asp	Pro 220	Asp	His	Phe	Ala
45	Gln 225	Arg	Gln	Ser	Cys 230	Met	Asn	Thr	Phe	Ala	Ser 235	Trp	Phe	Gly	Tyr	Met 240
50	Pro	Leu	Ile	His 245	Ser	Gln	Met	Arg	Leu	Asp 250	Pro	Val	Leu	Lys	Asp 255	Gln
	Val	Ser	Ile 260	Leu	Arg	Lys	Lys	Tyr	Arg 265	Asp	Ile	Glu	Arg	Leu 270		

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(B) TYPE: amino acid

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(2) INFORMATION FOR SEQ ID NO:15:

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTATGGCGAG TGACCCGACG TG

22

20 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35 TTGCTAAAGT GAAGGAAGTT GG

22

(2) INFORMATION FOR SEQ ID NO:18:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: DNA (genomic)

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCGACGTG ATCTGG

16

(2) INFORMATION FOR SEQ ID NO:19:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5AAGAGCTCCT GCAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTCTCGTTGC CCTCTCAC

18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCATCAATC TGTCACG

17

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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ACTACGATGA CCGGATC

17

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

"02660860" 0909920

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

18

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

AACATGGCTG ACAACG

16

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATTGGTGGT GGAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATCCAGCCA TGGTCTCCTT GG

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGTCGATGCC ATTATTACCA GC

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCCTTCCTC ATCACAG

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGTCTGTGT ATGCACTTGT G

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCGATGCC ATTATTACCA GC

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(2) INFORMATION FOR SEQ ID NO:31:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTCAAGGGTG TGGAGAG

17

20 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35 TTGGCTGAAA GCCAACAACC TG

22

(2) INFORMATION FOR SEQ ID NO:33:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AACATGCACG CATCCACAGC

20

(2) INFORMATION FOR SEQ ID NO:34:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

"02660360"

18

(2) INFORMATION FOR SEQ ID NO:35:

15 (ii) MOLECULE TYPE: DNA (genomic)

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GGTTCTGTCA GTATTAGCTG GG

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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21

TTCTCCCTC TGCTCATCCT C

40 (2) INFORMATION FOR SEQ ID NO:37:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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TTCCCACTCT GTCTCTC

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